

EMBL-EBI European Bioinformatics Institute

Get Nucleotide sequences for [] Site search []

Site Map SAS Start Session

EBI Home About EBI Research Services Training Data/Tools Download Submit

InterPro

InterPro home Text Search Sequence Search Databases Documentation FTP site Protein of the month

Search: [] Search Entries [] Search InterPro []

InterPro DNA mismatch repair protein

[?] = help

IPR002099 Matches: 147 proteins
DNA_mis_repair View matches: [\[Overview\]](#) [\[...sorted by Name\]](#) [\[of known structure\]](#) [\[Detailed view\]](#) [\[Table view\]](#)

Name [?] DNA mismatch repair protein

Signatures [?] PF01119;DNA_mis_repair (147 proteins)
PS00058;DNA_MISMATCH_REPAIR_1 (179 proteins)
TIGR00585;mull (124 proteins)

Type [?] Family

Dates [?] 1999-10-08 17:07:25.0 (created)
2001-07-03 14:39:47.0 (modified)

Contains [?] IPR003594; ATP-binding region, ATPase-like

Process [?] mismatch repair (GO:0006298)

Abstract [?] Mismatch repair contributes to the overall fidelity of DNA replication. It involves the correction of mismatched base pairs that have been missed by the proofreading element of the DNA polymerase complex [1]. The sequence of some proteins involved in mismatch repair in different organisms have been found to be evolutionary related.

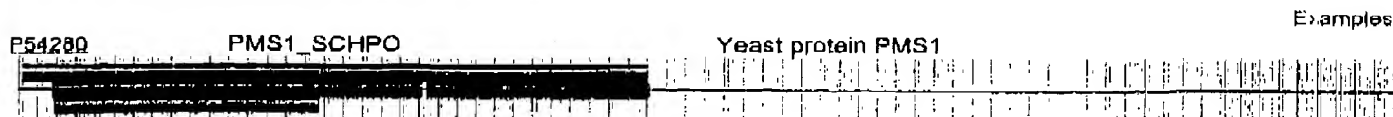
Structural links PDB 1b62, 1bkn, 1gg6, 1hzs
[?] CATH 3.30.230.10.4, 3.30.565.10
SCOP d.122.1.2, d.14.1.3

Database links Blocks IPR002099
[?] PROSITE doc PDOC00057

Taxonomy [?] 8 Saccharomyces cerevisiae
13 Fungi
2 Caenorhabditis elegans
2 Nematoda
36 Metazoa
6 Fruit Fly
6 Arthropoda
15 Chordata
6 Mouse
5 Human
48 Eukaryota




Unclassified
Virus
Archaea
Bacteria
Cyanobacteria
Synechocystis PCC 6803
Rice spp.
Arabidopsis thaliana
Green Plants
Plastid Group
Other Eukaryotes

3
96
4
1
1
6
7
12



P54279	PMS2_MOUSE	Mouse protein PSM2
P14161	MUTL_SALTY	mutL bacterial protein
P14160	HEXB_STRPN	Streptococcus pneumoniae hexB protein
P40692	MLH1_HUMAN	Human protein MLH1

[More proteins...](#)

[IPR002099](#) DNA mismatch repair protein 
[IPR003594](#) ATP-binding region, ATPase-like 
SuperFamily 

Publications

- Modrich P.
DNA mismatch correction.
Annu. Rev. Biochem. 56: 435- 466 (1987) [[PubMed: 3304141](#)]
- McIntyre C.A. , Mankovich J.A. , Walker G.C.
Nucleotide sequence of the Salmonella typhimurium mutL gene required for mismatch repair: homology of MutL to HexB of Streptococcus pneumoniae and to PMS1 of the yeast Saccharomyces cerevisiae.
J. Bacteriol. 171: 5325- 5331 (1989) [[PubMed: 2876972](#)]
- Prudhomme M. , Claverys J.-P. , Mejean V. , Martin B.
Nucleotide sequence of the Streptococcus pneumoniae hexB mismatch repair gene: homology of HexB to MutL of Salmonella typhimurium and to PMS1 of Saccharomyces cerevisiae.
J. Bacteriol. 171: 5332- 5338 (1989) [[PubMed: 2676973](#)]
- Bronner C.E. , Godwin A.R. , Tannergard P. , Linblom A. , Bollag R.J. , Lipford J. , Warren G. , Earlbino C. , Kar e M. , Lescoe M.K. , Kolodner R.D. , Smith L.G. , Fishel R. , Morrison P.T. , Baker S.M. , Nordenskjold M. , Liskay R.M. , Ward D.C.
Mutation in the DNA mismatch repair gene homologue hMLH1 is associated with hereditary non-polyposis colon cancer.
Nature 368: 258- 261 (1994) [[PubMed: 8145827](#)]


[Normal](#) [Printer Friendly](#) [Text](#) [Simple HTML](#) [XML](#) [Curator View](#)

Page Maintained by EBI Support.

SEQUENCE: Sequence 1 CRC64: 2A5289C333C7D8AA LENGTH: 724 aa	
InterPro IPR002099	DNA mismatch repair protein
Family PF01119	DNA mismatch repair protein, C-termina
TIGRFAMs TIGR00585	multi: DNA mismatch repair protein Muhl
PROSITE PS00058	DNA_MSMATCH_REPAIR_1
Parent	no parent
Children	no children
Found In	no entries
Contains	IPR003594
GO terms	Biological Process: mismatch repair (GO:0006298)
InterPro IPR003594	ATP-binding region, ATPase-like
Domain PF02518	Histidine kinase-, DNA gyrase B-, and
SMART SM00387	Histidine kinase-like ATPases
Parent	no parent
Children	IPR004358 IPR010194
Found in	IPR001241 IPR001404 IPR002099 IPR005467 IPR005734 IPR006290 IPR008358 IPR010193
Contains	no entries
GO terms	Molecular Function: ATP binding (GO:0005524)
noIPR unintegrated	unintegrated PD0000740

PRODOM	<u>Q8S2D3_EEEEE_Q8S2D3</u>	T
PRODOM	<u>PD002741</u>	3e-36 [274-346]T
PRODOM	<u>PD018003</u>	e-153 [347-625]T
PRODOM	<u>PD393849</u>	2e-35 [626-713]T
PRODOM	<u>PD641161</u>	2e-11 [209-214]T
PRODOM	<u>PD673298</u>	6e-26 [215-273]T
PIR	<u>PIRSF006464</u> no name	0 [1-724]T
SUPERFAMILY	<u>SSF54211</u>	7.7e-34 [225-349]T
SUPERFAMILY	<u>SSF55874</u>	5.2e-34 [14-224]T
Parent	no parent	
Children	no children	
Found in	no entries	
Contains	no entries	
GO terms	none	

Picture View Raw Output XML Output Original Source **Print Summary Another Job**

Page maintained by [EBI Support](#)
 [View Printer-friendly version of this page.](#)